## SEQUENCE LISTING

<110> Genentech, Inc. Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.

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- <150> PCT/US00/04414
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Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe 145 150 150 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln 180 185

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<213> Homo sapiens
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Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
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Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn 165 170 175

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             20
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Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
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Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65
Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                  85
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
             100
Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
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                             120
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2479

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn 225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg 245 250 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe 260 265 270

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu 275 280 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln 290 295 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp 305 310 315 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly 325 330 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu 340 345 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro 355 360 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro 370 375 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro 385 390 395 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

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Ala Tyr Lys 450	Leu	Thr	Trp	Val 455	Lys	Met	Gly	His	Ser 460	Leu	Val	Gly	Gly
Ile Val Gln 465	Glu	Arg	Ile 470	Val	Ser	Gly	Glu	Lys 475	Gln	His	Leu	Ser	Leu 480
Val Asn Leu	Glu	Pro 485	Arg	Ser	Thr	Tyr	Arg 490	Ile	Сув	Leu	Val	Pro 495	Leu
Asp Ala Phe	Asn 500	Tyr	Arg	Ala	Val	Glu 505	Asp	Thr	Ile	Cys	Ser 510	Glu	Ala
Thr Thr His 515	Ala	Ser	Tyr	Leu	Asn 520	Asn	Gly	Ser	Asn	Thr 525	Ala	Ser	Ser
His Glu Gln 530	Thr	Thr	Ser	His 535	Ser	Met	Gly	Ser	Pro 540	Phe	Leu	Leu	Ala
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Val Phe Cys	Trp	His 565	Met	His	Lys	Lys	Gly 570	Arg	Tyr	Thr	Ser	Gln 575	Lys
Trp Lys Tyr	Asn 580	Arg	Gly	Arg	Arg	Lys 585	Asp	Asp	Tyr	Cys	Glu 590	Ala	Gly
Thr Lys Lys 595	Asp	Asn	Ser	Ile	Leu 600	Glu	Met	Thr	Glu	Thr 605	Ser	Phe	Gln
Ile Val Ser 610	Leu				Gln						Phe	Arg	Leu
Gln Pro Ile 625	Tyr	Thr	Pro 630	Asn	Gly	Gly	Ile	Asn 635	Tyr	Thr	Asp	Cys	His 640
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<213> Homo sapiens

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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
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Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
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Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

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Phe 465	Ala	Cys	Gln	Cys	Pro 470	Glu	Gly	His	Val	Leu 475	Arg	Ser	Asp	Gly	Lys 480
Thr	Cys	Ala	Lys	Leu 485	Asp	Ser	Cys	Ala	Leu 490	Gly	Asp	His	Gly	Cys 495	Glu
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- Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val 515 520 525
- Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp 530 540
- Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp 545 550 555 560
- Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
  565 570 575
- Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys 580 585 590
- Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Cys 595 600 605
- Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser 610 615 620
- Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile 625 630 635 636
- Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu 645 650 655
- Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn 660 665 670
- Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly 675 680 685
- Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser 690 695 700
- Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg 705 710 715 720
- Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu 725 730 735
- Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
  740 745 750
- Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro 755 760 765
- Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu 770 775 780
- Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser 785 790 795 800

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Ser C	ys Sei 83!		Phe	Ala	Val	Gln 840	His	Arg	Tyr	Leu	Phe 845	Glu	Glu	Asp	
Asn Le	eu Lei 50	ı Arg	Ser	Thr	Gln 855	Lys	Leu	Ser	His	Ser 860	Thr	Lys	Pro	Ser	
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Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
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- Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Asn Lys Leu
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85

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Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr 180 185 190

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Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro 165 170 175

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gtcaagetea tegtgettgt geetecatee aageetacag ttaacateee etectetgee 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactett cetatgteet gaateeeaca acaggagage tggtetttga teecetgtea 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaatqctg tgcgcatgga agctgtggag cggaatgtgg gggtcatcgt ggcagccgtc 780
cttgtaaccc tgattctcct gggaatcttg gtttttggca tctggtttgc ctatagccga 840
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gctcaccqcc tatcatctqc atttqcctta ctcaqqtqct accqqactct qqcccctqat 1020
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teggatgtgt ttttaataat gteagetatg tgeeceatee teetteatge eeteecteee 1140
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<212> PRT
<213> Homo sapiens
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Leu Ala Ile Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
         35
                             40
                                                 45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
                         55
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65
                     70
                                         75
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Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
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<210> 122 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 122 acacctggtt caaagatggg	20
<210> 123 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 123 taggaagagt tgctgaaggc acgg	24
<210> 124 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 124 ttgccttact caggtgctac	20
<210> 125 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	

## oligonucleotide probe

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<400> 125
actcagcagt ggtaggaaag
                                                                   20
<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens
<400> 126
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gagogtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactaq 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tqcccaqqcc qcaqqcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
teacetggeg etgegaeagg gaettggaet geagegatgg eagegatgag gaggagtgea 300
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaaqaa actqcqcaac tqcaqccqcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tqactgcatt ccactcacqt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcqqc tqtqqaacca 540
atgagateet eeeggaaggg gatgeeacaa eeatggggee eeetgtgaee etggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actqcctatq 720
gggttattgc agetgetgeg gtgeteagtg caageetggt caeegecaee etecteettt 780
tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840
agtecetget getgteagaa cagaagaeet egetgeeetg aggaeaagea ettgeeacea 900
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gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020
teetgeagaa gtggeeetgg agattgaggg teeetggaca eteeetatgg agateegggg 1080
agetaggatg gggaacetge cacagecaga aetgagggge tggeeecagg cageteecag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc
                                                                  1210
<210> 127
<211> 282
<212> PRT
<213> Homo sapiens
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Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
                                 25
Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
         35
                             40
                                                 45
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
                     70
                                         75
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Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln 85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Leu Arg Asn Cys Ser 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

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<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 129
ttggttccac agccgagctc gtcg
                                                                   24
<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc
                                                                  50
<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (1837)
<223> a, t, c or g
<400> 131
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gggttagact ggcggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
cagactettg caagetggat geetetgtg gatgaaaqat gtateatqqa atqaaceeqa 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tcccccaga 240
gactettgge egtgateetg tggttteage tggegetgtg etteggeeet geacagetea 300
cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatggcttca 360
ggacccccag cggagggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgetga gatteataac aagacatata gacatggaga gaagetaate atcacttgte 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctqqtc qtccaqccca cccqqtqcc ttqctctqqa aqcccaaqtc tqtccactac 900
ctccaatggt gagtcacgga gatttcqtct qccacccqcq qccttqtqaq cqctacaacc 960
acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020
acateacetg ceagtatgga gagtggttte ettettatea agtetactge ateaaateag 1080
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcgttca 1140
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eggeaaceag tgtgetgetg gtgetgetge tegteateet ggeeaggatg tteeagacea 1200
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ctcccaggtg ccaagagagc acccacctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtgagggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa
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<211> 490
<212> PRT
<213> Homo sapiens
<400> 132
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                  5
                                     10
Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
             20
                                 25
Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
                             40
Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
                 85
                                     90
                                                         95
Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
                                105
Asp Asn Ser Ile Cys Val Glu Glu Asp Cys Arg Ile Pro Gln Ile Glu
                            120
Asp Ala Glu Ile His Asn Lys Thr Tyr Arq His Gly Glu Lys Leu Ile
                        135
    130
Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
                    150
                                        155
Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
                165
                                    170
                                                         175
Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn
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			180					185					190		
Ile	Ser	Glu 195	Leu	Gln	Thr	Ser	Phe 200	Pro	Val	Gly	Thr	Val 205	Ile	Ser	Tyr
Arg	Cys 210	Phe	Pro	Gly	Phe	Lys 215	Leu	Asp	Gly	Ser	Ala 220	Tyr	Leu	Glu	Cys
Leu 225	Gln	Asn	Leu	Ile	Trp 230	Ser	Ser	Ser	Pro	Pro 235	Arg	Cys	Leu	Ala	Leu 240
Glu	Ala	Gln	Val	Cys 245	Pro	Leu	Pro	Pro	Met 250	Val	Ser	His	Gly	Asp 255	Phe
Val	Cys	His	Pro 260	Arg	Pro	Cys	Glu	Arg 265	Tyr	Asn	His	Gly	Thr 270	Val	Val
Glu	Phe	Tyr 275	Cys	Asp	Pro	Gly	Tyr 280	Ser	Leu	Thr	Ser	Asp 285	Tyr	Lys	Tyr
Ile	Thr 290	Cys	Gln	Tyr	Gly	Glu 295	Trp	Phe	Pro	Ser	Tyr 300	Gln	Val	Tyr	Cys
Ile 305	Lys	Ser	Glu	Gln	Thr 310	Trp	Pro	Ser	Thr	His 315	Glu	Thr	Leu	Leu	Thr 320
Thr	Trp	Lys	Ile	Val 325	Ala	Phe	Thr	Ala	Thr 330	Ser	Val	Leu	Leu	Val 335	Leu
Leu	Leu	Val	Ile 340	Leu	Ala	Arg	Met	Phe 345	Gln	Thr	Lys	Phe	Lys 350	Ala	His
Phe	Pro	Pro 355	Arg	Gly	Pro	Pro	Arg 360	Ser	Ser	Ser	Ser	Asp 365	Pro	Asp	Phe
Val	Val 370	Val	Asp	Gly	Val	Pro 375	Val	Met	Leu	Pro	Ser 380	Tyr	Asp	Glu	Ala
Val 385	Ser	Gly	Gly	Leu	Ser 390	Ala	Leu	Gly	Pro	Gly 395	Tyr	Met	Ala	Ser	Val 400
Gly	Gln	Gly	Cys	Pro 405	Leu	Pro	Val	Asp	Asp 410	Gln	Ser	Pro	Pro	Ala 415	Tyr
Pro	Gly	Ser	Gly 420	Asp	Thr	Asp	Thr	Gly 425	Pro	Gly	Glu	Ser	Glu 430	Thr	Cys
Asp	Ser	Val 435	Ser	Gly	Ser	Ser	Glu 440	Leu	Leu	Gln	Ser	Leu 445	Tyr	Ser	Pro
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile

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Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
                    470
                                         475
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465
His Ala His Trp Val Leu Phe Leu Arg Asn
                485
<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 133
                                                                    23
atctcctatc gctgctttcc cgg
<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 134
agccaggatc gcagtaaaac tcc
                                                                    23
<210> 135
<211> 50
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 135
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<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens
<400> 136
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gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggeegt getgetggee gtgetgetgg tggggetgeg ggeegegaeg ggtegeetge 240
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300
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qqccttqtta taaaqtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaaqaaqc ctqcaqqaqq qatqqaqqcc aqctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcqaqqtctg cgtggtcatg taccatcage categgcace egetggcate ggaggeceet 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
qaqaaqctqc cttgaatctg gcctacatcc taatccccag cattcccctt ctcctccccc 900
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cagaccctag cacaaagaag caacacca tctggccctc tcctcaccag ggaaacagcc 1020
cqqacctaqa qqtctacaat qtcataagaa aacaaagcga agctgactta gctgagaccc 1080
qqccaqacct qaaqaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
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aaaqatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
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                                                                  1815
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<210> 137
<211> 382
<212> PRT
<213> Homo sapiens
<400> 137
Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
         35
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gln Leu Val Ser
 65
                     70
                                         75
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
```

- Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr 115 120 125
- Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser 130 135
- Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro 145 150 155 160
- Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys 165 170 175
- Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala 180 185 190
- Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro 195 200 205
- Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys 210 215 220
- Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser 225 230 235 240
- Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val 245 250 255
- Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys 260 265 270
- Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp 275 280 285
- Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala 290 295 300
- Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly 305 310 315 320
- Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val\$325\$ 330 335
- Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly 340 345 350
- Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg 355 360 365
- Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr 370 375 380

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 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe
  <400> 138
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 <210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe
<400> 139
                                                                    24
 aaqccaaaga agcctgcagg aggg
 <210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
  <223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe
  <400> 140
                                                                    24
 cagtccaagc ataaaggtcc tggc
  <210> 141
  <211> 1514
  <212> DNA
  <213> Homo sapiens
  <400> 141
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 gcatcegcag gttccegcgg acttgggggc gccegctgag ccceggcgcc cgcagaagac 120
  ttqtqtttqc ctcctqcaqc ctcaacccqq aqqqcaqcqa gggcctacca ccatgatcac 180
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Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly 225 230 235 240

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Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys 195 200 205

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Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp 225 230 235 240

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Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly 275 280 285

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Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

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	.> 24						•									
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~ZI3	, , Al		rcra-	י יסכו	10C110	~_										

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170

165

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- Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly 210 215 220
- Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr 225 230 235 240
- Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys 245 250 255
- Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His 260 265 270
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- Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr 355 360 365
- Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser 370 375 380
- Gin Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr 385 390 395 400
- His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala 405 410 415
- Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu 420 425 430
- Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
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  440
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- Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

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Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
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<sup>&</sup>lt;213> Homo sapiens

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- Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys 20 25 30
- Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met 35 40 45
- Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
  50 55 60
- Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp 65 70 75 80
- Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr 85 90 95
- Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr 100 105 110
- Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val 115 120 125
- Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe 130 135 140
- Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr 145 150 155 160
- Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu 165 170 175
- Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile 180 185 190
- Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys 195 200 205
- Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu 210 215 220
- Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser 225 230 235 240
- Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg 245 250 255
- Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr 260 265 270
- Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys 290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val 340 345 350

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His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu 485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys 500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg 530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu 545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

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- Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys 65 70 75 80
- Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro 85 90 95
- Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe 100 105 110
- Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr 115 120 125
- Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser 130 135 140
- Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp 145 150 155 160
- Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg 165 170 175
- Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu 180 185 190
- Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys 195 200 205
- Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val 210 215 220
- Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser 225 230 235 240
- Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr 245 250 255
- Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly 260 265 270
- Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro 275 280 285
- His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr 290 295 300
- Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val 305 310 315 320
- Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn 325 330 335

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Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
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Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
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Asn Val Ile
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Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
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Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
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<213> Homo sapiens
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<222> (977)
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Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
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Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
     50
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Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

75

70

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser 275 280 285

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<213> Artificial Sequence

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Pro 225	Ile	Met	Leu	Pro	Arg 230	Gln	Pro	Cys	Gly	Gly 235	Pro	Gly	Leu	Ala	Pro 240
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His	Pro	Glu 275	Lys	Leu	Thr	Leu	Thr 280	Glu	Ala	Arg	Glu	Ala 285	Cys	Gln	Glu
Asp	Asp 290	Ala	Thr	Ile	Ala	Lys 295	Val	Gly	Gln	Leu	Phe 300	Ala	Ala	Trp	Lys
Phe 305	His	Gly	Leu	Asp	Arg 310	Cys	Asp	Ala	Gly	Trp 315	Leu	Ala	Asp	Gly	Ser 320
Val	Arg	Tyr	Pro	Val 325		His	Pro	His	Pro 330		Cys	Gly	Pro	Pro 335	
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Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
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Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly 225 230 235 240

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- His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile 355 360 365
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- Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala 420 425 430
- Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp 435 440 445
- Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser 450 455 460
- Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp 465 470 475 480
- Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile 485 490 495
- Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met 500 505 510
- Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr 515 520 525
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Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe 50 55 60

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Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

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Asn	Asp	Phe	Ala	Phe 110	Met	Leu	His	Leu	Ile 115	Asp	Gln	Tyr	Asp	Pro 120
Leu	Tyr	Ser	Lys	Arg 125	Phe	Ala	Val	Phe	Leu 130	Ser	Glu	Val	Ser	Glu 135
Asn	Lys	Leu	Arg	Gln 140	Leu	Asn	Leu	Asn	Asn 145	Glu	Trp	Thr	Leu	Asp 150
Lys	Leu	Arg	Gln	Arg 155	Leu	Thr	Lys	Asn	Ala 160	Gln	Asp	Lys	Leu	Glu 165
Leu	His	Leu	Phe	Met 170	Leu	Ser	Gly	Ile	Pro 175	Asp	Thr	Val	Phe	Asp 180
Leu	Val	Glu	Leu	Glu 185	Val	Leu	Lys	Leu	Glu 190	Leu	Ile	Pro	Asp	Val 195
Thr	Ile	Pro	Pro	Ser 200	Ile	Ala	Gln	Leu	Thr 205	Gly	Leu	Lys	Glu	Leu 210
Trp	Leu	Tyr	His	Thr 215	Ala	Ala	Lys	Ile	Glu 220	Ala	Pro	Ala	Leu	Ala 225
Phe	Leu	Arg	Glu	Asn 230	Leu	Arg	Ala	Leu	His 235	Ile	Lys	Phe	Thr	Asp 240
Ile	Lys	Glu	Ile	Pro 245	Leu	Trp	Ile	Tyr	Ser 250	Leu	Lys	Thr	Leu	Glu 255
Glu	Leu	His	Leu	Thr 260	Gly	Asn	Leu	Ser	Ala 265	Glu	Asn	Asn	Arg	Tyr 270
Ile	Val	Ile	Asp	Gly 275	Leu	Arg	Glu	Leu	Lys 280	Arg	Leu	Lys	Val	Leu 285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp
				290					295					300
Val	Gly	Val	His	Leu 305	Gln	Lys	Leu	Ser	Ile 310	Asn	Asn	Glu	Gly	Thr 315
Lys	Leu	Ile	Val	Leu 320	Asn	Ser	Leu	Lys	Lys 325	Met	Ala	Asn	Leu	Thr 330
Glu	Leu	Glu	Leu	Ile 335	Arg	Cys	Asp	Leu	Glu 340	Arg	Ile	Pro	His	Ser 345
Ile	Phe	Ser	Leu	His 350	Asn	Leu	Gln	Glu	Ile 355	Asp	Leu	Lys	Asp	Asn 360

<400> 251

<210> 252 <211> 24

caacaatgag ggcaccaagc 20

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile 380 385 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu 400 395 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys 415 410 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe 430 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala 445 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln 460 455 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile 490 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp 520 515 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg 530 Ala Asp Lys Glu Gln Ala <210> 251 <211> 20 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe

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<223> Synthetic Oligonucleotide Probe
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<212> DNA
<213> Homo Sapien
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gegetetece gteeegeggt ggttgetget getgeegetg etgetgggee 100
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250
 ggcttcaggg cggtccaggc ggttctagca ctggatttgg aaactttgag 300
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
 ccaggetgec agteteetat ttgtggataa tecegtggge actgggttea 400
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
 cagetggeat tggtetagag etttataagg ceatteageg agggaceate 600
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctcccctgt 650
 tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700
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<sup>&</sup>lt;210> 255

<sup>&</sup>lt;211> 452

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu 1 5 10 15

Leu Leu Pro Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr 110 115 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu 125 130 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser 160 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly 185 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys 215 220 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala 230 235 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys 245 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr 260 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser 275 280 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His 290 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

	305	310	315
Pro Ile Arg Lys	Lys Leu Lys 320	Ile Ile Pro Glu A	Asp Gln Ser Trp 330
Gly Gly Gln Ala	Thr Asn Val	Phe Val Asn Met G	Glu Glu Asp Phe 345
Met Lys Pro Val	Ile Ser Ile	Val Asp Glu Leu I	eu Glu Ala Gly
	350	355	360
Ile Asn Val Thr	Val Tyr Asn	Gly Gln Leu Asp I	eu Ile Val Asp
	365	370	375
Thr Met Gly Glr	Glu Ala Trp	Val Arg Lys Leu I	ys Trp Pro Glu
	380	385	390
Leu Pro Lys Phe	Ser Gln Leu	Lys Trp Lys Ala I	Leu Tyr Ser Asp
	395	400	405
Pro Lys Ser Leu	Glu Thr Ser	Ala Phe Val Lys S	Ser Tyr Lys Asn
	410	415	420
Leu Ala Phe Tyr	Trp Ile Leu	Lys Ala Gly His N	Met Val Pro Ser
	425	430	435
Asp Gln Gly Asp	Met Ala Leu	Lys Met Met Arg I	eu Val Thr Gln
	440	445	450
Gln Glu			
<210> 256 <211> 1100			

<400> 256

<212> DNA

<213> Homo Sapien

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550 tacatcaaaa aggatgaggc actgccatct ccccacaccc tccaggaagt 600 tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700 caaggcggga aggatgcctg cttcggtgac tcaggtggac ccttggcctg 750 tacacaagaat ggactgtgt atcagattga tcaggtggac ccttggcctg 750 taacaagaat ggactgtgt atcagattgac tcaggtggac tggggagtgg 800 gctgtggtcg cccaatcgg cccggtgtct acaccaatat cagccaccac 850 tttgagtgac tcagaagct gatggcccag agtggcatgt cccagccaga 900 cccctcctgg ccactactct ttttccctct tctctgggct ctcccactcc 950 tgggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000 agtcaggccc tggttcttct ctgtcttgtt tggtaataaa cacattccag 1050 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaa aaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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Ala Gly Leu Arq Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu 80 85 90

Ser Asp	Pro	Ser	Gly 95	Trp	Met	Val	Gln	Phe 100	Gly	Gln	Leu	Thr	Ser 105
Met Pro	Ser	Phe	Trp 110	Ser	Leu	Gln	Ala	Tyr 115	Tyr	Thr	Arg	Tyr	Phe 120
Val Ser	Asn	Ile	Tyr 125	Leu	Ser	Pro	Arg	Tyr 130	Leu	Gly	Asn	Ser	Pro 135
Tyr Asp	Ile	Ala	Leu 140	Val	Lys	Leu	Ser	Ala 145	Pro	Val	Thr	Tyr	Thr 150
Lys His	Ile	Gln	Pro 155	Ile	Cys	Leu	Gln	Ala 160	Ser	Thr	Phe	Glu	Phe 165
Glu Asn	Arg	Thr	Asp 170	Cys	Trp	Val	Thr	Gly 175	Trp	Gly	Tyr	Ile	Lys 180
Glu Asp	Glu	Ala	Leu 185	Pro	Ser	Pro	His	Thr 190	Leu	Gln	Glu	Val	Gln 195
Val Ala	Ile	Ile	Asn 200	Asn	Ser	Met	Cys	Asn 205	His	Leu	Phe	Leu	Lys 210
Tyr Ser	Phe	Arg	Lys 215	Asp	Ile	Phe	Gly	Asp 220	Met	Val	Cys	Ala	Gly 225
Asn Ala	Gln	Gly	Gly 230	Lys	Asp	Ala	Cys	Phe 235	Gly	Asp	Ser	Gly	Gly 240
Pro Leu	Ala	Cys	Asn 245	Lys	Asn	Gly	Leu	Trp 250	Tyr	Gln	Ile	Gly	Val 255
Val Ser	Trp	Gly	Val 260	Gly	Cys	Gly	Arg	Pro 265	Asn	Arg	Pro	Gly	Val 270
Tyr Thr	Asn	Ile	Ser 275	His	His	Phe	Glu	Trp 280	Ile	Gln	Lys	Leu	Met 285
Ala Gln	Ser	Gly	Met 290	Ser	Gln	Pro	Asp	Pro 295	Ser	Trp	Pro	Leu	Leu 300
Phe Phe	Pro	Leu	Leu 305	Trp	Ala	Leu	Pro	Leu 310	Leu	Gly	Pro	Val	

<sup>&</sup>lt;210> 258

<sup>&</sup>lt;211> 2427

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 258

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cctcctaggg ctctttgccc tcatcctctc tggcaaatgc agttacagcc 100 cggagcccga ccagcggagg acgctgccc caggctgggt gtccctgggc 150 cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200 gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250 ctcctcaata cggaaaatac ctgaccctag agaatgtggc tgatctggtg 300 aggecatece caetgaceet ecaeaeggtg caaaaatgge tettggeage 350 cggagcccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400 ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagtttcat 450 cactatgtgg gaggacctac ggaaacccat gttgtaaggt ccccacatcc 500 ctaccagett ccacaggeet tggeceecca tgtggaettt gtggggggae 550 tgcaccgttt tcccccaaca tcatccctga ggcaacgtcc tgagccgcag 600 gtgacaggga ctgtaggect gcatctgggg gtaaccccct ctgtgatccg 650 taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700 acagccaagc ctgtgcccag ttcctggagc agtatttcca tgactcagac 750 ctggctcagt tcatgcgcct cttcggtggc aactttgcac atcaggcatc 800 ccagtctaga tgtgcagtac ctgatgagtg ctggtgccaa catctccacc 900 tgggtctaca gtagccctgg ccggcatgag ggacaggagc ccttcctgca 950 gtggctcatg ctgctcagta atgagtcagc cctgccacat gtgcatactg 1000 tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050 gtcaacactg agetcatgaa ggetgeeget eggggtetea eeetgetett 1100 cgcctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150 agttccgccc taccttccct gcctccagcc cctatgtcac cacagtggga 1200 ggcacatect tecaggaace ttteeteate acaaatgaaa ttgttgaeta 1250 tatcagtggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300 aggaagctgt aacgaagttc ctgagctcta gcccccacct gccaccatcc 1350 agttacttca atgccagtgg ccgtgcctac ccagatgtgg ctgcactttc 1400

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Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu 1 5 10 15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

<sup>&</sup>lt;210> 259

<sup>&</sup>lt;211> 556

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

<sup>&</sup>lt;400> 259

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Leu	Pro	Pro	Gly	Trp 35	Val	Ser	Leu	Gly	Arg 40	Ala	Asp	Pro	Glu	Glu 45
Glu	Leu	Ser	Leu	Thr 50	Phe	Ala	Leu	Arg	Gln 55	Gln	Asn	Val	Glu	Arg 60
Leu	Ser	Glu	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr	Gly	Lys	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro	Ser	Pro	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala	Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala	Glu	Phe	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165
His	Val	Asp	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu	His	Leu	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu	Thr	Ser	Gln	Asp 215	Val	Gly	Ser	Gly	Thr 220	Ser	Asn	Asn	Ser	Gln 225
Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser	Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile	Glu	Ala	Ser	Leu 275	Asp	Val	Gln	Tyr	Leu 280	Met	Ser	Ala	Gly	Ala 285

Asn	Ile	Ser	Thr	Trp 290	Val	Tyr	Ser	Ser	Pro 295	Gly	Arg	His	Glu	Gly 300
Gln	Glu	Pro	Phe	Leu 305	Gln	Trp	Leu	Met	Leu 310	Leu	Ser	Asn	Glu	Ser 315
Ala	Leu	Pro	His	Val 320	His	Thr	Val	Ser	Tyr 325	Gly	Asp	Asp	Glu	Asp 330
Ser	Leu	Ser	Ser	Ala 335	Tyr	Ile	Gln	Arg	Val 340	Asn	Thr	Glu	Leu	Met 345
Lys	Ala	Ala	Ala	Arg 350	Gly	Leu	Thr	Leu	Leu 355	Phe	Ala	Ser	Gly	Asp 360
Ser	Gly	Ala	Gly	Cys 365	Trp	Ser	Val	Ser	Gly 370	Arg	His	Gln	Phe	Arg 375
Pro	Thr	Phe	Pro	Ala 380	Ser	Ser	Pro	Tyr	Val 385	Thr	Thr	Val	Gly	Gly 390
Thr	Ser	Phe	Gln	Glu 395	Pro	Phe	Leu	Ile	Thr 400	Asn	Glu	Ile	Val	Asp 405
Tyr	Ile	Ser	Gly	Gly 410	Gly	Phe	Ser	Asn	Val 415	Phe	Pro	Arg	Pro	Ser 420
Tyr	Gln	Glu	Glu	Ala 425	Val	Thr	Lys	Phe	Leu 430	Ser	Ser	Ser	Pro	His 435
Leu	Pro	Pro	Ser	Ser 440	Tyr	Phe	Asn	Ala	Ser 445	Gly	Arg	Ala	Tyr	Pro 450
Asp	Val	Ala	Ala	Leu 455	Ser	Asp	Gly	Tyr	Trp 460	Val	Val	Ser	Asn	Arg 465
Val	Pro	Ile	Pro	Trp 470	Val	Ser	Gly	Thr	Ser 475	Ala	Ser	Thr	Pro	Val 480
Phe	Gly	Gly	Ile	Leu 485	Ser	Leu	Ile	Asn	Glu 490	His	Arg	Ile	Leu	Ser 495
Gly	Arg	Pro	Pro	Leu 500	Gly	Phe	Leu	Asn	Pro 505	Arg	Leu	Tyr	Gln	Gln 510
His	Gly	Ala	Gly	Leu 515	Phe	Asp	Val	Thr	Arg 520	Gly	Cys	His	Glu	Ser 525
Cys	Leu	Asp	Glu	Glu 530	Val	Glu	Gly	Gln	Gly 535	Phe	Cys	Ser	Gly	Pro 540
Gly	Trp	Asp	Pro	Val 545	Thr	Gly	Trp	Gly	Thr 550	Pro	Thr	Ser	Gln	Leu 555

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<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

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<210> 261 <211> 383 <212> PRT

<213> Homo Sapien

<400> 261

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Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro 20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr 35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu 50 55 60

Val Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu 65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu 80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

95 100 105

Leu Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser 110 115 120

Ser	Gly	Lys	Ser	Arg 125	Arg	Lys	Arg	Gln	Ile 130	Tyr	Gly	Tyr	Asp	Ser 135
Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Cys	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240
Ile	Gly	Met	Asp	Tyr 245	Asp	Tyr	Ala	Leu	Leu 250	Glu	Leu	Lys	Lys	Pro 255
His	Lys	Arg	Lys	Phe 260	Met	Lys	Ile	Gly	Val 265	Ser	Pro	Pro	Ala	Lys 270
Gln	Leu	Pro	Gly	Gly 275	Arg	Ile	His	Phe	Ser 280	Gly	Tyr	Asp	Asn	Asp 285
Arg	Pro	Gly	Asn	Leu 290	Val	Tyr	Arg	Phe	Cys 295	Asp	Val	Lys	Asp	Glu 300
Thr	Tyr	Asp	Leu	Leu 305	Tyr	Gln	Gln	Cys	Asp 310	Ala	Gln	Pro	Gly	Ala 315
Ser	Gly	Ser	Gly	Val 320	Tyr	Val	Arg	Met	Trp 325	Lys	Arg	Gln	Gln	Gln 330
Lys	Trp	Glu	Arg	Lys 335	Ile	Ile	Gly	Ile	Phe 340	Ser	Gly	His	Gln	Trp 345
Val	Asp	Met	Asn	Gly 350	Ser	Pro	Gln	Asp	Phe 355	Asn	Val	Ala	Val	Arg 360
Ile	Thr	Pro	Leu	Lys 365	Tyr	Ala	Gln	Ile	Cys 370	Tyr	Trp	Ile	Lys	Gly 375
Asn	Tyr	Leu	Asp	Cys 380	Arg	Glu	Gly							

<210> 262 <211> 1378 <212> DNA

<213> Homo Sapien

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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263 Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Cys Leu Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu 95 Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys 130 Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp

175

180

170

<211> 24

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Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
                                     205
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
                                     220
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
                                     250
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
                                     280
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
                                     295
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
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Arg Ser
<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 264
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<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 265
 gcagaggtgt ctaaggttg 19
<210> 266
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<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 266
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<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 267
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<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 268
 ggggaattca ccctatgaca ttgcc 25
<210> 269
<211> 24
<212> DNA
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 <223> Synthetic Oligonucleotide Probe
 <400> 269
 gaatgccctg caagcatcaa ctgg 24
 <210> 270
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic Oligonucleotide Probe
 <400> 270
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<210> 271
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<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 271
gcggaagggc agaatgggac tccaag 26
<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 272
cagccctgcc acatgtgc 18
<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 273
tactgggtgg tcagcaac 18
<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 274
ggcgaagagc agggtgagac cccg 24
<210> 275
<211> 45
<212> DNA
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<223> Synthetic Oligonucleotide Probe
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<400> 275
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<210> 276
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<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 276
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<210> 277
<211> 18
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe
<400> 277
 ggctatgaca gcaggttc 18
<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 278
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 <210> 279
 <211> 24
 <212> DNA
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 <223> Synthetic Oligonucleotide Probe
 <400> 279
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<223> Synthetic Oligonucleotide Probe
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<211> 61
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<213> Artificial Sequence
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<400> 282
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<210> 283
<211> 119
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ggaetgeaca eegggeeeae aceteteetg eeeeteete etgagteetg 1650
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala 35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val 65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe
80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu 95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys 110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala 125 130 135

Lys	Thr	Glu	Arg	Ile 140	Gly	Cys	Gly	Ser	His 145	Phe	Cys	Glu	Lys	Leu 150
Gln	Gly	Val	Glu	Glu 155	Thr	Asn	Ile	Glu	Leu 160	Leu	Val	Cys	Asn	Tyr 165
Glu	Pro	Pro	Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr	Pro	Cys	Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Cys	Lys	Asn	Ser 195
Leu	Cys	Glu	Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr	Leu	Val	Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp	Ser	Arg	Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
			Leu	245					250					255
			Ala	260					265					270
			Pro	275					280					285
			Pro	290					295					300
			Pro	305					310					315
			Ala	320					325					330
				335	•				340					345
				350	١				355					360
				365	;				370					9 Pro 375
				380	)				385	,				390
Gly	r His	Thi	ser Ser	Ser 395		s Sei	Leu	ı Pro	Asr 400		Pro	Asr	1 Thr	405

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Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
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<400> 287
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<212> DNA
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Ala	Asn	Ile	Thr	Leu 65	Leu	Ser	Leu	Ala	Gly 70	Asn	Arg	Ile	Val	Glu 75
Ile	Leu	Pro	Glu	His 80	Leu	Lys	Glu	Phe	Gln 85	Ser	Leu	Glu	Thr	Leu 90
Asp	Leu	Ser	Ser	Asn 95	Asn	Ile	Ser	Glu	Leu 100	Gln	Thr	Ala	Phe	Pro 105
Ala	Leu	Gln	Leu	Lys 110	Tyr	Leu	Tyr	Leu	Asn 115	Ser	Asn	Arg	Val	Thr 120
Ser	Met	Glu	Pro	Gly 125	Tyr	Phe	Asp	Asn	Leu 130	Ala	Asn	Thr	Leu	Leu 135
Val	Leu	Lys	Leu	Asn 140	Arg	Asn	Arg	Ile	Ser 145	Ala	Ile	Pro	Pro	Lys 150
Met	Phe	Lys	Leu	Pro 155	Gln	Leu	Gln	His	Leu 160	Glu	Leu	Asn	Arg	Asn 165
Lys	Ile	Lys	Asn	Val 170	Asp	Gly	Leu	Thr	Phe 175	Gln	Gly	Leu	Gly	Ala 180
Leu	Lys	Ser	Leu	Lys 185	Met	Gln	Arg	Asn	Gly 190	Val	Thr	Lys	Leu	Met 195
Asp	Gly	Ala	Phe	Trp 200	Gly	Leu	Ser	Asn	Met 205	Glu	Ile	Leu	Gln	Leu 210
Asp	His	Asn	Asn	Leu 215	Thr	Glu	Ile	Thr	Lys 220	Gly	Trp	Leu	Tyr	Gly 225
Leu	Leu	Met	Leu	Gln 230	Glu	Leu	His	Leu	Ser 235	Gln	Asn	Ala	Ile	Asn 240
Arg	Ile	Ser	Pro	Asp 245	Ala	Trp	Glu	Phe	Cys 250	Gln	Lys	Leu	Ser	Glu 255
Leu	Asp	Leu	Thr	Phe 260	Asn	His	Leu	Ser	Arg 265	Leu	Asp	Asp	Ser	Ser 270
Phe	Leu	Gly	Leu	Ser 275	Leu	Leu	Asn	Thr	Leu 280	His	Ile	Gly	Asn	Asn 285
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Phe	Thr	Gly	Leu	Asp 350	Ala	Leu	Glu	His	Leu 355	Asp	Leu	Ser	Asp	Asn 360
Ala	Ile	Met	Ser	Leu 365	Gln	Gly	Asn	Ala	Phe 370	Ser	Gln	Met	Lys	Lys 375
Leu	Gln	Gln	Leu	His 380	Leu	Asn	Thr	Ser	Ser 385	Leu	Leu	Cys	Asp	Cys 390
Gln	Leu	Lys	Trp	Leu 395	Pro	Gln	Trp	Val	Ala 400	Glu	Asn	Asn	Phe	Gln 405
Ser	Phe	Val	Asn	Ala 410	Ser	Cys	Ala	His	Pro 415	Gln	Leu	Leu	Lys	Gly 420
Arg	Ser	Ile	Phe	Ala 425	Val	Ser	Pro	Asp	Gly 430	Phe	Val	Cys	Asp	Asp 435
Phe	Pro	Lys	Pro	Gln 440	Ile	Thr	Val	Gln	Pro 445	Glu	Thr	Gln	Ser	Ala 450
Ile	Lys	Gly	Ser	Asn 455	Leu	Ser	Phe	Ile	Cys 460	Ser	Ala	Ala	Ser	Ser 465
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
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Leu	His	Asp	Ala	Glu 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495
Gly	Gly	Glu	Val	Met 500	Glu	Tyr	Thr	Thr	Ile 505	Leu	Arg	Leu	Arg	Glu 510
Val	Glu	Phe	Ala	Ser 515	Glu	Gly	Lys	Tyr	Gln 520	Cys	Val	Ile	Ser	Asn 525
His	Phe	Gly	Ser	Ser 530	Tyr	Ser	Val	Lys	Ala 535	Lys	Leu	Thr	Val	Asn 540
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Ala	Gly	Ala	Met	Ala 560	Arg	Leu	Glu	Cys	Ala 565	Ala	Val	Gly	His	Pro 570
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Ala	Ala	Arg	Glu	Arg 590	Arg	Met	His	Val	Met 595	Pro	Glu	Asp	Asp	Val 600
Phe	Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	Asp 610	Ile	Gly	Val	Tyr	Ser 615
Cys	Thr	Ala	Gln	Asn 620	Ser	Ala	Gly	Ser	Ile 625	Ser	Ala	Asn	Ala	Thr 630
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Gly	Gly	Ser	Pro	Pro 665	Pro	Lys	Leu	Asn	Trp 670	Thr	Lys	Asp	Asp	Ser 675
Pro	Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690
Leu	Leu	Ile	Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705
Thr	Cys	Glu	Met	Ser 710	Asn	Thr	Leu	Gly	Thr 715	Glu	Arg	Gly	Asn	Val 720
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Trp	Val	Val	Ile	Ile 770	Tyr	His	Thr	Arg	Arg 775	Arg	Asn	Glu	Asp	Cys 780
Ser	Ile	Thr	Asn		Asp	Glu	Thr	Asn		Pro	Ala	Asp	Ile	
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Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser 820 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr 855 845 850 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His 880 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr 890 Glu Pro Ser Tyr Ile Lys Lys Glu Cys Tyr Pro Cys Ser His 905 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp 925 930 Pro Ser His Val Arq Lys Leu Leu Asn Thr Ser Tyr Ser His Asn 935 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu 955 950 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn 965 970 975 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu 985 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg 995 1000 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly 1010 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn 1030 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro 1050 1040 1045 Asn Phe Gln Ser Tyr Asp Leu Asp Thr

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35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser 65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile 80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu 95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe 110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg 125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

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Leu Se	r Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu Ile	e Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu Se	r Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly Le	ı Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln Va	l Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu Il	e Asn	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu Ph	e Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn Pro	o Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
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Arg Al	a Ser	Thr	Ser 380	Leu	Thr	Ser	Val	Ser 385	Trp	Ile	Thr	Pro	Asn 390
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Phe	Ser	Tyr	Phe	Ser 455	Thr	Val	Thr	Val	Glu 460	Thr	Met	Glu	Pro	Ser 465
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Val	Asp	Asp	Glu	Ile 575	Thr	Gly	Asp	Thr	Pro 580	Met	Glu	Ser	His	Leu 585
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Tyr	Lys	Ser	Pro	Phe 605	Asn	His	Thr	Thr	Thr 610	Val	Asn	Thr	Ile	Asn 615
Ser	Ile	His	Ser	Ser 620	Val	His	Glu	Pro	Leu 625	Leu	Ile	Arg	Met	Asn 630
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<211> 4053

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Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys 80 85 90

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45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
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Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met

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Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met 110  $\phantom{000}$  115  $\phantom{000}$  120

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Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg 140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg 155 160 165

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Lys	Cys	His	Lys	Gly 200	Phe	Asp	Leu	Met	Tyr 205	Ile	Gly	Gly	Lys	Tyr 210
Gln	Cys	His	Asp	Ile 215	Asp	Glu	Cys	Ser	Leu 220	Gly	Gln	Tyr	Gln	Cys 225
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Pro	Pro	Pro	Leu	Pro 335	Thr	Glu	Leu	Arg	Thr 340	Pro	Leu	Pro	Pro	Thr 345
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Thr	Asp	Pro	Gln	Lys 380	Pro	Arg	Gly	Asp	Val 385		Ser	Val	Leu	Val 390
His	Ser	Cys	Asn	Phe 395		His	Gly	Leu	Cys 400		Trp	Ile	Arg	Glu 405
Lys	Asp	Asn	. Asp			Trp	Glu	Pro			Asp	Pro	Ala	Gly 420
al.	. 07:	m ·	т	410		C 0	. 7\ J ~	7. T. A.	415		Dro	, G137	ريا ته	
GTA	Gln	Tyr	ьeu	ınr	٧al	ser	AId	AId	пув	TIC	FIC	. GTĀ	OTA	цy

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Pro	Asn	Ala	Ser	Leu 95	Leu	Ile	Asn	Pro	Leu 100	Gln	Phe	Pro	Asp	Glu 105
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Phe	Asp	Cys	Ser	Ala 260	Asp	Ser	His	Pro	Pro 265		Thr	Tyr	Ser	Trp 270
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Arg	Leu	Glu	Val	Ala 290		Glu	Lys	Val	Ala 295		Lys	Thr	Met	Asp 300
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Pro	Asp	Val	Ser	Gly 410	Val	Ser	Arg	Ile	Pro 415	Ser	Arg	Ser	Val	Pro 420
Ala	Ser	Asp	Cys	Val 425	Ser	Gly	Gln	Asp	Leu 430	His	Ser	Thr	Val	Tyr 435
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 acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
 ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
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 ccaacaaaat ggaagcettg actagcaagt cagetgetga tgetgaggge 400
 tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450
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 gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600
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  gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750
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/つ・	ın	`	って	2	2

- <212> PRT
- <213> Homo Sapien

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Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val 80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu 95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg 110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala 125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile 140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser 155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly 170 175 180

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<sup>&</sup>lt;211> 533

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Ala	Leu	Glu	Leu	Thr 230	Arg	Arg	Leu	Leu	Ser 235	Leu	Asp	Pro	Ser	His 240
Glu	Arg	Ala	Gly	Gly 245	Asn	Leu	Arg	Tyr	Phe 250	Glu	Gln	Leu	Leu	Glu 255
Glu	Glu	Arg	Glu	Lys 260	Thr	Leu	Thr	Asn	Gln 265	Thr	Glu	Ala	Glu	Leu 270
Ala	Thr	Pro	Glu	Gly 275	Ile	Tyr	Glu	Arg	Pro 280	Val	Asp	Tyr	Leu	Pro 285
Glu	Arg	Asp	Val	Tyr 290	Glu	Ser	Leu	Cys	Arg 295	Gly	Glu	Gly	Val	Lys 300
Leu	Thr	Pro	Arg	Arg 305	Gln	Lys	Arg	Leu	Phe 310	Cys	Arg	Tyr	His	His 315
Gly	Asn	Arg	Ala	Pro 320	Gln	Leu	Leu	Ile	Ala 325	Pro	Phe	Lys	Glu	Glu 330
Asp	Glu	Trp	Asp	Ser 335	Pro	His	Ile	Val	Arg 340	Tyr	Tyr	Asp	Val	Met 345
Ser	Asp	Glu	Glu	Ile 350	Glu	Arg	Ile	Lys	Glu 355	Ile	Ala	Lys	Pro	Lys 360
Leu	Ala	Arg	Ala	Thr 365	Val	Arg	Asp	Pro	Lys 370	Thr	Gly	Val	Leu	Thr 375
Val	Ala	Ser	Tyr	Arg 380	Val	Ser	Lys	Ser	Ser 385	Trp	Leu	Glu	Glu	Asp 390
Asp	Asp	Pro	Val	<b>Val</b> 395	Ala	Arg	Val	Asn	Arg 400	Arg	Met	Gln	His	Ile 405
Thr	Gly	Leu	Thr	Val 410	Lys	Thr	Ala	Glu	Leu 415	Leu	Gln	Val	Ala	Asn 420
Tyr	Gly	Val	Gly	Gly 425	Gln	Tyr	Glu	Pro	His 430	Phe	Asp	Phe	Ser	Arg 435
Arg	Pro	Phe	Asp	Ser 440		Leu	Lys	Thr	Glu 445	Gly	Asn	Arg	Leu	Ala 450
Thr	Phe	Leu	Asn	Tyr 455		Ser	Asp	Val	Glu 460		Gly	· Gly	Ala	Thr 465
Val	Phe	Pro	Asp	Leu 470		Ala	Ala	. Ile	Trp 475		Lys	Lys	Gly	Thr 480

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Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
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Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro 1 5 10 15

Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg 20 25 30

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Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg 80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

				95					100					105
Val	Leu	Thr	Ser	Arg 110	Ala	Thr	Leu	Ser	Thr 115	Leu	Ala	Val	Ala	Val 120
Asn	Arg	Thr	Val	Ala 125	His	His	Phe	Pro	Arg 130	Leu	Leu	Tyr	Phe	Thr 135
Gly	Gln	Arg	Gly	Ala 140	Arg	Ala	Pro	Ala	Gly 145	Met	Gln	Val	Val	Ser 150
His	Gly	Asp	Glu	Arg 155	Pro	Ala	Trp	Leu	Met 160	Ser	Glu	Thr	Leu	Arg 165
His	Leu	His	Thr	His 170	Phe	Gly	Ala	Asp	Tyr 175	Asp	Trp	Phe	Phe	Ile 180
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Ala	Gly	His	Leu	Ser 200	Ile	Asn	Gln	Asp	Leu 205	Tyr	Leu	Gly	Arg	Ala 210
Glu	Glu	Phe	Ile	Gly 215	Ala	Gly	Glu	Gln	Ala 220	Arg	Tyr	Cys	His	Gly 225
Gly	Phe	Gly	Tyr	Leu 230	Leu	Ser	Arg	Ser	Leu 235	Leu	Leu	Arg	Leu	Arg 240
Pro	His	Leu	Asp	Gly 245	Cys	Arg	Gly	Asp	Ile 250	Leu	Ser	Ala	Arg	Pro 255
Asp	Glu	Trp	Leu	Gly 260	Arg	Cys	Leu	Ile	Asp 265	Ser	Leu	Gly	Val	Gly 270
Cys	Val	Ser	Gln	His 275	Gln	Gly	Gln	Gln	Туr 280	Arg	Ser	Phe	Glu	Leu 285
Ala	Lys	Asn	Arg	Asp 290	Pro	Glu	Lys	Glu	Gly 295	Ser	Ser	Ala	Phe	Leu 300
Ser	Ala	Phe	Ala	Val 305	His	Pro	Val	Ser	Glu 310		Thr	Leu	Met	Tyr 315
Arg	Leu	His	Lys	Arg 320	Phe	Ser	Ala	Leu	Glu 325		Glu	Arg	Ala	Tyr 330
Ser	Glu	Ile	Glu	Gln 335	Leu	Gln	Ala	Gln	340		Asn	Leu	Thr	Val 345
Leu	Thr	Pro	Glu	Gly 350		Ala	Gly	Leu	Ser 355		Pro	Val	Gly	Leu 360

Pro	Ala	Pro	Phe	Thr 365	Pro	His	Ser	Arg	Phe 370	Glu	Val	Leu	Gly	Trp 375
Asp	Tyr	Phe	Thr	Glu 380	Gln	His	Thr	Phe	Ser 385	Cys	Ala	Asp	Gly	Ala 390
Pro	Lys	Cys	Pro	Leu 395	Gln	Gly	Ala	Ser	Arg 400	Ala	Asp	Val	Gly	Asp 405
Ala	Leu	Glu	Thr	Ala 410	Leu	Glu	Gln	Leu	Asn 415	Arg	Arg	Tyr	Gln	Pro 420
Arg	Leu	Arg	Phe	Gln 425	Lys	Gln	Arg	Leu	Leu 430	Asn	Gly	Tyr	Arg	Arg 435
Phe	Asp	Pro	Ala	Arg 440	Gly	Met	Glu	Tyr	Thr 445	Leu	Asp	Leu	Leu	Leu 450
Glu	Cys	Val	Thr	Gln 455	Arg	Gly	His	Arg	Arg 460	Ala	Leu	Ala	Arg	Arg 465
	Ser			470					475					480
	Tyr			485					490					495
	Val			500					505					510
	Ala			515					520					525
				530					535					Asp 540
				545					550					Arg 555
_				560					565					Ala 570
				575					580					Pro 585
				590					595					600
				605					610					Trp 615
Gln	. Ala	Phe	Phe	620		His	Phe	Gln	Glu 625		. Asr	Pro	Ala	Leu 630

Ser	Pro	Gln	Arg	Ser 635	Pro	Pro	Gly	Pro	Pro 640	Gly	Ala	Gly	Pro	Asp 645
Pro	Pro	Ser	Pro	Pro 650	Gly	Ala	Asp	Pro	Ser 655	Arg	Gly	Ala	Pro	Ile 660
Gly	Gly	Arg	Phe	Asp 665	Arg	Gln	Ala	Ser	Ala 670	Glu	Gly	Cys	Phe	Tyr 675
Asn	Ala	Asp	Tyr	Leu 680	Ala	Ala	Arg	Ala	Arg 685	Leu	Ala	Gly	Glu	Leu 690
Ala	Gly	Gln	Glu	Glu 695	Glu	Glu	Ala	Leu	Glu 700	Gly	Leu	Glu	Val	Met 705
Asp	Val	Phe	Leu	Arg 710	Phe	Ser	Gly	Leu	His 715	Leu	Phe	Arg	Ala	Val 720
Glu	Pro	Gly	Leu	Val 725	Gln	Lys	Phe	Ser	Leu 730	Arg	Asp	Cys	Ser	Pro 735
Arg	Leu	Ser	Glu	Glu 740	Leu	Tyr	His	Arg	Cys 745	Arg	Leu	Ser	Asn	Leu 750
Glu	Gly	Leu	Gly	Gly 755	Arg	Ala	Gln	Leu	Ala 760	Met	Ala	Leu	Phe	Glu 765
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<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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<sup>&</sup>lt;210> 341

<sup>&</sup>lt;211> 318

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Homo Sapien

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Gly	His	Gly	Asn	Arg 35	Met	His	His	His	Glu 40	His	His	His	Leu	Gln 45
Ala	Pro	Asn	Lys	Glu 50	Asp	Ile	Leu	Lys	Ile 55	Ser	Glu	Asp	Glu	Arg 60
Met	Glu	Leu	Ser	Lys 65	Ser	Phe	Arg	Val	туr 70	Cys	Ile	Ile	Leu	Val 75
Lys	Pro	Lys	Asp	Val 80	Ser	Leu	Trp	Ala	Ala 85	Val	Lys	Glu	Thr	Trp 90
Thr	Lys	His	Cys	Asp 95	Lys	Ala	Glu	Phe	Phe 100	Ser	Ser	Glu	Asn	Val 105
Lys	Val	Phe	Glu	Ser 110	Ile	Asn	Met	Asp	Thr 115	Asn	Asp	Met	Trp	Leu 120
Met	Met	Arg	Lys	Ala 125	Tyr	Lys	Tyr	Ala	Phe 130	Asp	Lys	Tyr	Arg	Asp 135
Gln	Tyr	Asn	Trp	Phe 140	Phe	Leu	Ala	Arg	Pro 145	Thr	Thr	Phe	Ala	Ile 150
Ile	Glu	Asn	Leu	Lys 155		Phe	Leu	Leu	Lys 160	Lys	Asp	Pro	Ser	Gln 165
Pro	Phe	Tyr	Leu	Gly 170		Thr	Ile	Lys	Ser 175		Asp	Leu	Glu	Tyr 180
Val	Gly	Met	Glu	Gly 185		Ile	Val	Leu	Ser 190		Glu	Ser	Met	Lys 195
Arg	Leu	Asn	Ser	Leu 200		Asn	Ile	Pro	Glu 205		Cys	Pro	Glu	Gln 210
Gly	Gly	Met	lle	215		Ile	Ser	Glu	. Asp 220		Gln	Leu	Ala	Val 225
Cys	Leu	Lys	Tyr	230		Val	Phe	Ala	Glu 235		Ala	Glu	. Asp	Ala 240
Asp	Gly	Lys	s Asp	Val 245		. Asn	Thr	Lys	Ser 250		. Gly	/ Leu	Ser	: Ile 255
Lys	Glu	Alā	a Met	Thr	Tyr	His	Pro	Asn	ı Glr	ı Val	. Val	Glu	Gly	cys Cys

270

260 265 Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln 275 Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly 290 His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser 310 Asp Asn Asp <210> 342 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 342 tececaagee gttetagaeg egg 23 <210> 343 <211> 18 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 343 ctggttcttc cttgcacg 18 <210> 344 <211> 28 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 344 gcccaaatgc cctaaggcgg tatacccc 28 <210> 345 <211> 50 <212> DNA <213> Artificial Sequence <220>

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 atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
 ctctcctgct acaattatgq atcaggttca gtcaagaatt gttgtccatt 350
 gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400
 tttcctggqc gttaagttta aagaactgct cagccatggg ggctcacctg 450
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 taaaatgaga gagtttttta ttggactgtc agaccaggtt gtcgagggtc 550
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 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
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Met Asn Ser Ser Lys Ser Ser Glu Thr Gln Cys Thr Glu Arg Gly
1 5 10 15

Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro  $20 \hspace{1cm} 25 \hspace{1cm} 30$ 

Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser 80 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
95 100 105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser 110 115 120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg 125 130 135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp 140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala 170 175 180

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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
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                 185
Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
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gggatgtggt gaacacagaa ca 22
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ettetteetg etgetgettt teaggggetg eetgataggg getgtaaate 150
 tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
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Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
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Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
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Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly

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Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val 140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
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Leu	Ala	Leu	Ile	Thr 260	Leu	Gly	Ile	Cys	Cys 265	Ala	Tyr	Arg	Arg	Gly 270
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